



SEQUENCE LISTING

<110> Osteryoung, Katherine W.

<120> Manipulation of Min Genes in Plants

<130> 920905.90041

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<150> 60/130,403

<151> 1999-04-19

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

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<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(978)

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cca tca tct ctc tca caa aag act cta ata tct tca cca aga ttc gtc	96
Pro Ser Ser Leu Ser Gln Lys Thr Leu Ile Ser Ser Pro Arg Phe Val	
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aat aac cct agc aga cgg agt cca ata cga tcc gtt ctt caa ttt aat	144
Asn Asn Pro Ser Arg Arg Ser Pro Ile Arg Ser Val Leu Gln Phe Asn	
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cgc aaa ccg gaa ctc gcc gga gaa acg ccg cgt atc gtc gtt atc acc	192
Arg Lys Pro Glu Leu Ala Gly Glu Thr Pro Arg Ile Val Val Ile Thr	
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tcc gga aaa ggc ggt gtt gga aag acg aca acc acc gca aat gtc ggt	240
Ser Gly Lys Gly Gly Val Gly Lys Thr Thr Thr Ala Asn Val Gly	
65 70 75 80	
ctc tct ctc gct cgt tac ggt ttc tca gtt gtc gcc att gac gcc gac	288
Leu Ser Leu Ala Arg Tyr Gly Phe Ser Val Val Ala Ile Asp Ala Asp	
85 90 95	
ctt ggt ctc cgt aac ctc gat ctc ctc cta ggg tta gag aat cga gtc	336
Leu Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu Asn Arg Val	
100 105 110	
aat tac act tgc gtc gag gtt ata aac gga gat tgt cgt ctc gat caa	384
Asn Tyr Thr Cys Val Glu Val Ile Asn Gly Asp Cys Arg Leu Asp Gln	
115 120 125	

gct ctg gta cgt gat aag cgt tgg tcg aat ttc gaa ttg cta tgt ata 432
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 130 135 140

tct aaa cct aga tcg aaa ctt ccg atg gga ttt ggt ggt aaa gca ttg 480
 Ser Lys Pro Arg Ser Lys Leu Pro Met Gly Phe Gly Gly Lys Ala Leu
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gaa tgg ctt gtg gat gcg ttg aaa act aga ccg gaa ggt tca ccg gat 528
 Glu Trp Leu Val Asp Ala Leu Lys Thr Arg Pro Glu Gly Ser Pro Asp
 165 170 175

ttc atc atc atc gat tgt cct gca gga atc gat gcc gga ttc ata acc 576
 Phe Ile Ile Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe Ile Thr
 180 185 190

gcc att act ccg gcg aat gaa gca gtt ctg gta aca act ccg gat ata 624
 Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro Asp Ile
 195 200 205

aca gcg tta agg gat gct gat agg gtt acg ggt ttg tta gaa tgc gat 672
 Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu Cys Asp
 210 215 220

gga atc aga gat ata aag atg att gtg aac aga gtg aga act gat atg 720
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 225 230 235 240

att aaa gga gag gat atg atg tca gtg tta gat gtg cag gag atg ttg 768
 Ile Lys Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu Met Leu
 245 250 255

gga ttg tca ttg ctt ggt gta att cct gaa gat tct gag gtt att cga 816
 Gly Leu Ser Leu Leu Gly Val Ile Pro Glu Asp Ser Glu Val Ile Arg
 260 265 270

agc acg aat cga ggg ttt ccg ctt gtt ctg aat aag cct cct acg ctt 864
 Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr Leu
 275 280 285

gcg gga ttg gcg ttt gag cag gcg gct tgg aga ctc gtt gag caa gat 912
 Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln Asp
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agt atg aag gct gtt atg gtg gag gaa gaa cct aag aaa cgt ggc ttc 960
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 35 40 45

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Ser Gly Lys Gly Gly Val Gly Lys Thr Thr Thr Thr Ala Asn Val Gly
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Leu Ser Leu Ala Arg Tyr Gly Phe Ser Val Val Ala Ile Asp Ala Asp
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Leu Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu Asn Arg Val
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Asn Tyr Thr Cys Val Glu Val Ile Asn Gly Asp Cys Arg Leu Asp Gln
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Glu Trp Leu Val Asp Ala Leu Lys Thr Arg Pro Glu Gly Ser Pro Asp
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Phe Ile Ile Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe Ile Thr
 180 185 190

Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro Asp Ile
 195 200 205

Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu Cys Asp
 210 215 220

Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr Asp Met
 225 230 235 240

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 260 265 270

Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr Leu
 275 280 285

Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln Asp
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aca ttc aat ccc cta cac aaa acc cta act aaa cca aca cca aaa ccc 154
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tac cca aag cca cca cca att cgc tcc gtc ctt caa tac aat cgc aaa 202
 Tyr Pro Lys Pro Pro Pro Ile Arg Ser Val Leu Gln Tyr Asn Arg Lys
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 Val Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu Asn Arg Val
 70 75 80

aat tac acc gtc gtt gaa gtt ctc aac ggc gat tgc aga ctc gac caa 346
 Asn Tyr Thr Val Val Glu Val Leu Asn Gly Asp Cys Arg Leu Asp Gln
 85 90 95

gcc cta gtt cgt gat aaa cgc tgg tca aat ttc gaa ttg ctt tgt att 394
 Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu Leu Cys Ile
 100 105 110 115

tca aaa cct agg tca aaa ttg cct tta gga ttt ggg gga aaa gct tta 442
 Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly Lys Ala Leu
 120 125 130

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 Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys Pro Asp Phe
 135 140 145

ata ctt ata gat tgt cct gca ggt att gat gcc ggg ttc ata acc gcc 538
 Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe Ile Thr Ala
 150 155 160

att aca ccg gct aac gaa gcc gta tta gtt aca aca cct gat att act 586
 Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro Asp Ile Thr
 165 170 175

gca ttg aga gat gca gat aga gtt aca ggc ttg ctt gaa tgt gat gga 634
 Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu Cys Asp Gly
 180 185 190 195
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 Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr Asp Leu Ile
 200 205 210
 agg ggt gaa gat atg atg tca gtt ctt gat gtt caa gag atg ttg gga 730
 Arg Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu Met Leu Gly
 215 220 225
 ttg tca ttg ttg agt gat acc cga gga ttc gaa gtg att cgg agt acg 778
 Leu Ser Leu Leu Ser Asp Thr Arg Gly Phe Glu Val Ile Arg Ser Thr
 230 235 240
 aat aga ggg ttt ccg ctt gtg ttg aac aag cct ccg act tta gca gga 826
 Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr Leu Ala Gly
 245 250 255
 ttg gca ttt gag cag gct gct tgg aga ttg gtt gag caa gat agc atg 874
 Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln Asp Ser Met
 260 265 270 275
 aag gct gtg atg gtg gag gaa gaa cct aaa aag agg gga ttt ttc tcg 922
 Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly Phe Phe Ser
 280 285 290
 ttt ttt gga ggt tagtgatcga attcgttgaa tcgttgagtt gggtttgttt 974
 Phe Phe Gly Gly
 295
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 Asn Arg Lys Pro Glu Leu Ala Gly Asp Thr Pro Arg Val Val Ala Ile
 50 55 60
 Asp Ala Asp Val Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu
 65 70 75 80

Asn Arg Val Asn Tyr Thr Val Val Glu Val Leu Asn Gly Asp Cys Arg
 85 90 95
 Leu Asp Gln Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu
 100 105 110
 Leu Cys Ile Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly
 115 120 125
 Lys Ala Leu Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys
 130 135 140
 Pro Asp Phe Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe
 145 150 155 160
 Ile Thr Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro
 165 170 175
 Asp Ile Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu
 180 185 190
 Cys Asp Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr
 195 200 205
 Asp Leu Ile Arg Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu
 210 215 220
 Met Leu Gly Leu Ser Leu Leu Ser Asp Thr Arg Gly Phe Glu Val Ile
 225 230 235 240
 Arg Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr
 245 250 255
 Leu Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln
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 Phe Phe Ser Phe Phe Gly Gly
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<212> DNA

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